

PALM INTRANET

Day : Tuesday
Date: 10/17/2006

Time: 10:11:47

10/7/71 296

Inventor Name Search

Enter the **first few letters** of the Inventor's Last Name.
Additionally, enter the **first few letters** of the Inventor's First name.

Last Name

First Name

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Day : Tuesday
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Enter the **first few letters** of the Inventor's Last Name.
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Last Name

First Name

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SCORE Search Results Details for Application 10717296 and Search Result us-10-717-296-307.rag.

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OM protein - protein search, using sw model

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Run on:      October 14, 2006, 10:08:40 ; Search time 198 Seconds
              (without alignments)
              1166.133 Million cell updates/sec
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Title: US-10-717-296-307
Perfect score: 2690
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	2690	100.0	505	5	ADU01526	Adu01526 Breast ca
4	2690	100.0	505	5	ADZ41790	Adz41790 Human bre
5	2685	99.8	505	5	AAU83606	Aau83606 Human PRO
6	2685	99.8	505	5	ADY31770	Ady31770 Novel hum
7	2685	99.8	505	6	ABU10221	Abu10221 Human cyt
8	2685	99.8	505	6	ABU80753	Abu80753 Human PRO
9	2685	99.8	505	6	ABO33719	Abo33719 Novel hum
10	2685	99.8	505	6	ABU82062	Abu82062 Novel hum
11	2685	99.8	505	6	ABJ72242	Abj72242 Human PRO
12	2685	99.8	505	6	ABJ72370	Abj72370 Human PRO
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22	2685	99.8	505	7	ADB84651	Adb84651 Human PRO
23	2685	99.8	505	7	ADB83766	Adb83766 Novel hum
24	2685	99.8	505	7	ADB72921	Adb72921 Novel hum
25	2685	99.8	505	7	ADC36759	Adc36759 Human PRO
26	2685	99.8	505	7	ADC21749	Adc21749 Human PRO
27	2685	99.8	505	7	AAE39879	Aae39879 Human cyt
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ALIGNMENTS

RESULT 1

ABJ05536

ID ABJ05536 standard; protein; 505 AA.

XX

AC ABJ05536;

XX

DT 14-NOV-2002 (first entry)

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1	1465.5	54.5	510	2	US-09-852-067-2	Sequence 2, Appli
2	1465.5	54.5	510	2	US-10-338-691-2	Sequence 2, Appli
3	1391	51.7	489	2	US-09-852-067-4	Sequence 4, Appli
4	1391	51.7	489	2	US-10-338-691-4	Sequence 4, Appli
5	1310	48.7	444	2	US-10-104-047-2690	Sequence 2690, Ap
6	1017	37.8	520	3	US-10-114-270-60	Sequence 60, Appl
7	1005	37.4	524	2	US-09-976-594-533	Sequence 533, App
8	994	37.0	524	2	US-09-991-181-264	Sequence 264, App
9	994	37.0	524	2	US-09-990-444-264	Sequence 264, App
10	994	37.0	524	2	US-09-997-333-264	Sequence 264, App
11	994	37.0	524	2	US-09-992-598-264	Sequence 264, App
12	994	37.0	524	2	US-09-989-735-264	Sequence 264, App
13	994	37.0	524	3	US-09-989-726-264	Sequence 264, App
14	994	37.0	524	3	US-09-997-514-264	Sequence 264, App
15	994	37.0	524	3	US-09-989-728-264	Sequence 264, App
16	994	37.0	524	3	US-09-997-349-264	Sequence 264, App
17	994	37.0	524	3	US-09-997-653-264	Sequence 264, App
18	994	37.0	524	3	US-09-989-293A-264	Sequence 264, App
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21	651.5	24.2	314	2	US-10-104-047-2794	Sequence 2794, Ap
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23	543.5	20.2	520	3	US-09-992-901-2	Sequence 2, Appli
24	487.5	18.1	503	2	US-09-583-447A-2	Sequence 2, Appli
25	478.5	17.8	508	2	US-09-949-016-8561	Sequence 8561, Ap
26	478	17.8	504	2	US-09-583-447A-4	Sequence 4, Appli
27	469.5	17.5	508	2	US-09-949-016-7092	Sequence 7092, Ap
28	469.5	17.5	508	2	US-09-949-016-8562	Sequence 8562, Ap
29	464	17.2	504	2	US-09-502-426B-24	Sequence 24, Appl
30	463.5	17.2	503	2	US-09-144-367-2	Sequence 2, Appli
31	437	16.2	502	2	US-09-949-016-5992	Sequence 5992, Ap
32	437	16.2	507	2	US-09-949-016-7091	Sequence 7091, Ap
33	430	16.0	576	2	US-08-948-564-16	Sequence 16, Appl
34	416.5	15.5	504	1	US-08-457-274A-25	Sequence 25, Appl
35	416.5	15.5	504	5	PCT-US95-05758-25	Sequence 25, Appl
36	413	15.4	510	3	US-10-021-425-36	Sequence 36, Appl
37	389	14.5	526	1	US-08-298-426-4	Sequence 4, Appli
38	385.5	14.3	498	1	US-08-457-274A-24	Sequence 24, Appl
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ALIGNMENTS

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US-09-852-067-2

; Sequence 2, Application US/09852067

; Patent No. 6531297

; GENERAL INFORMATION:

; APPLICANT: MERKULOV, Gennady et al

; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

1	2690	100.0	505	3	US-09-910-689-307	Sequence 307, App
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7	2685	99.8	505	4	US-10-227-884-30	Sequence 30, Appl
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19	2685	99.8	505	4	US-10-219-003-30	Sequence 30, Appl
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ALIGNMENTS

RESULT 1

US-09-910-689-307

; Sequence 307, Application US/09910689

; Patent No. US20020081609A1

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; APPLICANT: Day, Craig H.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Wang, Tongtong

SCORE Search Results Details for Application 10717296 and Search Result us-10-717-296-307.rapbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM protein - protein search, using sw model

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Run on:      October 14, 2006, 10:20:10 ; Search time 39 Seconds .
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Perfect score: 2690
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Gapop 10.0 , Gapext 0.5

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                  Maximum Match 100%
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SUMMARIES

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4	1349	50.1	508	7	US-11-293-697-4775	Sequence 4775, Ap
5	1236.5	46.0	511	7	US-11-090-997-136	Sequence 136, App
6	1180.5	43.9	511	7	US-11-090-997-1026	Sequence 1026, Ap
7	994	37.0	524	6	US-10-196-749-204	Sequence 204, App
8	994	37.0	524	7	US-11-101-316-54	Sequence 54, Appl
9	994	37.0	524	7	US-11-376-673-54	Sequence 54, Appl
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11	543.5	20.2	520	7	US-11-056-355B-49170	Sequence 49170, A
12	538	20.0	493	7	US-11-056-355B-49171	Sequence 49171, A
13	525.5	19.5	456	7	US-11-056-355B-49172	Sequence 49172, A
14	487.5	18.1	503	6	US-10-532-868-13	Sequence 13, Appl
15	478.5	17.8	503	6	US-10-532-868-15	Sequence 15, Appl
16	470.5	17.5	430	7	US-11-056-355B-81092	Sequence 81092, A
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18	470.5	17.5	515	7	US-11-056-355B-81090	Sequence 81090, A
19	470	17.5	517	6	US-10-449-902-37190	Sequence 37190, A
20	469.5	17.5	503	6	US-10-527-603-53	Sequence 53, Appl
21	468.5	17.4	518	7	US-11-056-355B-19391	Sequence 19391, A
22	468.5	17.4	530	7	US-11-056-355B-19390	Sequence 19390, A
23	468.5	17.4	586	7	US-11-056-355B-19389	Sequence 19389, A
24	464	17.2	503	6	US-10-532-868-10	Sequence 10, Appl
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27	462	17.2	496	6	US-10-953-349-21310	Sequence 21310, A
28	462	17.2	496	7	US-11-056-355B-53642	Sequence 53642, A
29	462	17.2	523	6	US-10-953-349-21309	Sequence 21309, A
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31	462	17.2	523	7	US-11-317-789A-247	Sequence 247, App
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33	462	17.2	524	7	US-11-056-355B-53640	Sequence 53640, A
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35	459	17.1	503	6	US-10-532-868-18	Sequence 18, Appl
36	456.5	17.0	451	7	US-11-330-403-9778	Sequence 9778, Ap
37	456.5	17.0	498	7	US-11-056-355B-83653	Sequence 83653, A
38	456.5	17.0	511	7	US-11-056-355B-83652	Sequence 83652, A
39	456.5	17.0	512	7	US-11-056-355B-83651	Sequence 83651, A
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41	451	16.8	524	6	US-10-953-349-21297	Sequence 21297, A
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43	451	16.8	533	6	US-10-953-349-21296	Sequence 21296, A
44	451	16.8	533	7	US-11-056-355B-60224	Sequence 60224, A
45	449.5	16.7	502	6	US-10-532-868-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-10-540-310-4

; Sequence 4, Application US/10540310

; Publication No. US20060166212A1

; GENERAL INFORMATION:

; APPLICANT: Avalon Pharmaceuticals, Inc.

; TITLE OF INVENTION: Breast Specific Protein Expressed in Cancer and Methods of

; TITLE OF INVENTION: Use Thereof

; FILE REFERENCE: 689290-183

SCORE Search Results Details for App

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This page gives you Search Results detail for the Application 10717296 and Search Result us-10-7: [start](#)

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OM protein - protein search, using sw model

Run on: October 14, 2006, 10:13:15 ; Search time 43 Seconds
(without alignments)
1129.988 Million cell updates/sec

Title: US-10-717-296-307
Perfect score: 2690
Sequence: 1 MEPSWLQELMAHPFLLLILL.....VRQVVLKSKNGIHVFAKKVC 505

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
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3	1361.5	50.6	519	2 JX0331	laurate omega-hydr
4	1359.5	50.5	519	2 I53015	fatty acid omega-h
5	1357.5	50.5	509	1 O4RTL0	laurate omega-hydr
6	1351.5	50.2	511	1 A34260	laurate omega-hydr
7	1347.5	50.1	511	1 B34160	cytochrome P450 4A
8	1338	49.7	508	1 A36304	cytochrome P450 4A

9	1333.5	49.6	591	2	I65981	fatty acid omega-h
10	1333	49.6	510	1	A34160	laurate omega-hydr
11	1330.5	49.5	509	2	S47553	cytochrome P450 Cy
12	1305.5	48.5	507	1	A32966	cytochrome P450 4A
13	1301	48.4	504	1	A32965	cytochrome P450 4A
14	1236.5	46.0	511	2	S66472	cytochrome P450 4B
15	1219	45.3	506	1	A40164	cytochrome P450 4B
16	1205	44.8	511	1	B40164	cytochrome P450 4B
17	1189.5	44.2	515	1	JE0361	cytochromes P450,
18	1180.5	43.9	511	1	O4HUB1	cytochrome P450 4B
19	1016	37.8	520	2	S45702	leukotriene-B4 20-
20	1004	37.3	522	2	JC4532	cytochrome P450 4F
21	994	37.0	524	2	JC7594	cytochrome P450 en
22	994	37.0	524	2	JC7598	cytochrome P450 en
23	990	36.8	524	2	S29723	cytochrome P450 4F
24	966	35.9	520	1	A46661	leukotriene B4 ome
25	953	35.4	537	2	JC4534	cytochrome P450 4F
26	920	34.2	526	2	JC4533	cytochrome P450 4F
27	660	24.5	512	2	T13611	hypothetical prote
28	649.5	24.1	511	1	A39381	cytochrome P450 4
29	648	24.1	515	2	JC8026	cytochrome P450 en
30	628.5	23.4	511	1	S25707	cytochrome P450 4D
31	628	23.3	467	2	T21236	hypothetical prote
32	619	23.0	496	1	S41192	cytochrome P450 4D
33	600.5	22.3	513	2	JC7120	cytochrome P450 en
34	574.5	21.4	499	2	T18699	hypothetical prote
35	559	20.8	503	1	S66374	cytochrome P450 4M
36	545.5	20.3	509	2	T21512	hypothetical prote
37	543.5	20.2	503	2	T24985	hypothetical prote
38	543.5	20.2	520	2	H84663	probable cytochrom
39	535	19.9	524	2	T20471	hypothetical prote
40	526	19.6	485	1	JC5236	cytochrome P450, C
41	513.5	19.1	574	2	JC7327	cytochrome P450 en
42	505	18.8	141	2	S35610	cytochrome P450 4A
43	500	18.6	141	2	S35611	cytochrome P450 4A
44	488.5	18.2	583	2	T15644	probable cytochrom
45	487.5	18.1	503	2	JC7627	cytochrome P450 3A

ALIGNMENTS

RESULT 1

JC7883

cytochrome P450 4X1 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 05-Oct-2004

C;Accession: JC7883

R;Bylund, J.; Zhang, C.; Harder, D.R.

Biochem. Biophys. Res. Commun. 296, 677-684, 2002

A;Title: Identification of a novel cytochrome P450, CYP4X1, with unique localization s

A;Reference number: JC7883; MUID:22165495; PMID:12176035

A;Accession: JC7883

A;Molecule type: mRNA

A;Residues: 1-507

A;Cross-references: UNIPROT:Q8K4D6; UNIPARC:UPI00000E837D; GB:AF439343

C;Comment: This enzyme, which is a brain specific cytochrome P450 isoform belonging to

C;Genetics:

A;Gene: cyp4x1

C;Superfamily: human cytochrome P450 CYP4B1

5	1494	55.5	507	2	Q6A152_MOUSE	Q6a152	mus musculu
6	1476	54.9	509	1	CP4X1_HUMAN	Q8n118	homo sapien
7	1476	54.9	509	2	Q5VVE5_HUMAN	Q5vve5	homo sapien
8	1468	54.6	499	2	Q8BYS0_MOUSE	Q8bys0	mus musculu
9	1459	54.2	292	2	Q66ZJ5_HUMAN	Q66zj5	homo sapien
10	1403	52.2	510	2	Q2VHZ9_CANFA	Q2vhz9	canis famil
11	1388	51.6	510	1	CP4A4_RABIT	P10611	oryctolagus
12	1383	51.4	510	2	Q2VHZ7_CANFA	Q2vhz7	canis famil
13	1382	51.4	510	2	Q2VHZ8_CANFA	Q2vhz8	canis famil
14	1361.5	50.6	509	2	Q5EBD8_RAT	Q5ebd8	rattus norv
15	1361.5	50.6	519	1	CP4AB_HUMAN	Q02928	homo sapien
16	1361.5	50.6	519	2	Q5VSP8_HUMAN	Q5vsp8	homo sapien
17	1360	50.6	508	1	CP4AC_RAT	P24464	rattus norv
18	1357.5	50.5	509	1	CP4AA_RAT	P08516	rattus norv
19	1349.5	50.2	511	1	CP4A5_RABIT	P14579	oryctolagus
20	1346	50.0	510	1	CP4A6_RABIT	P14580	oryctolagus
21	1343.5	49.9	509	1	CP4AA_MOUSE	O88833	mus musculu
22	1341.5	49.9	511	1	CP4A7_RABIT	P14581	oryctolagus
23	1339	49.8	504	2	Q9GJX5_PIG	Q9gjx5	sus scrofa
24	1338.5	49.8	516	2	Q5RFC5_PONPY	Q5rfc5	pongo pygma
25	1338.5	49.8	519	2	Q6JXK8_HUMAN	Q6jxk8	homo sapien
26	1338.5	49.8	519	2	Q5R5F7_PONPY	Q5r5f7	pongo pygma
27	1334	49.6	508	1	CP4AC_MOUSE	Q91wl5	mus musculu
28	1332.5	49.5	521	2	Q16802_HUMAN	Q16802	homo sapien
29	1332	49.5	504	2	Q8SPK1_PIG	Q8spk1	sus scrofa
30	1329	49.4	504	2	Q8SPK0_PIG	Q8spk0	sus scrofa
31	1327.5	49.3	519	2	Q6JXK7_HUMAN	Q6jxk7	homo sapien
32	1327	49.3	504	2	Q95JF8_PIG	Q95jf8	sus scrofa
33	1324.5	49.2	515	2	Q4QQR3_XENTR	Q4qqr3	xenopus tro
34	1310	48.7	444	2	Q8NAZ3_HUMAN	Q8naz3	homo sapien
35	1309	48.7	508	2	Q6ZN67_HUMAN	Q6zn67	homo sapien
36	1309	48.7	510	2	Q5XG47_XENLA	Q5xg47	xenopus lae
37	1306.5	48.6	519	2	Q5TCH4_HUMAN	Q5tch4	homo sapien
38	1305.5	48.5	507	1	CP4AE_RAT	P20817	rattus norv
39	1305.5	48.5	519	2	Q9NRM4_HUMAN	Q9nrm4	homo sapien
40	1305	48.5	500	2	Q8HYL5_PHACI	Q8hyl5	phascolarct
41	1301	48.4	504	1	CP4A2_RAT	P20816	rattus norv
42	1301	48.4	504	2	Q4G071_RAT	Q4g071	rattus norv
43	1287.5	47.9	507	1	CP4AE_MOUSE	O35728	mus musculu
44	1275	47.4	501	2	Q9PVV8_XENLA	Q9pvv8	xenopus lae
45	1237.5	46.0	496	2	Q6AZQ1_XENLA	Q6azq1	xenopus lae

ALIGNMENTS

RESULT 1

CP4Z1_HUMAN

ID CP4Z1_HUMAN STANDARD; PRT; 505 AA.

AC Q86W10;

DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.

DT 01-JUN-2003, sequence version 1.

DT 07-FEB-2006, entry version 25.

DE Cytochrome P450 4Z1 (EC 1.14.14.1) (CYPIVZ1).

GN Name=CYP4Z1; ORFNames=UNQ3060/PRO9882;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

10/7171296

Qy	61	YPVKEFEVYHKLMEKYPCAVPLWVGPFMTFFSVHDPDYAKILLKRQDPKSAVSHKILES	120
Db	61	YPVKEFEVYHKLMEKYPCAVPLWVGPFMTFFSVHDPDYAKILLKRQDPKSAVSHKILES	120
Qy	121	VGRGLVTLDGSKWKHKRQIVKPGFNISILKIFITMMSESVRMLNKWEERIAQNSRLELF	180
Db	121	VGRGLVTLDGSKWKHKRQIVKPGFNISILKIFITMMSESVRMLNKWEERIAQNSRLELF	180
Qy	181	QHVSLMTLDSIMKCAFSHQSGSIQLDSTLDSYLKAVFNLSKISNQRMNLFHNDLVFKFS	240
Db	181	QHVSLMTLDSIMKCAFSHQSGSIQLDSTLDSYLKAVFNLSKISNQRMNLFHNDLVFKFS	240
Qy	241	SQQQIFSKFNQELHQFTEKVIQDRKESLKDCLKQDTTQKRRWDFLDILLSAKSENTKDFS	300
Db	241	SQQQIFSKFNQELHQFTEKVIQDRKESLKDCLKQDTTQKRRWDFLDILLSAKSENTKDFS	300
Qy	301	EADLQAEVKTFMFAGHDTTSSAISWILYCLAKYPEHQRCRDEIRELLGDGSSITWEHLS	360
Db	301	EADLQAEVKTFMFAGHDTTSSAISWILYCLAKYPEHQRCRDEIRELLGDGSSITWEHLS	360
Qy	361	QMPYTTMCIKECLRLYAPVVNISRLLDKPITFPDGRSLPAGITVFINIWALHHNPYFWED	420
Db	361	QMPYTTMCIKECLRLYAPVVNISRLLDKPITFPDGRSLPAGITVFINIWALHHNPYFWED	420
Qy	421	PQVFNPLRFSRENSSEKIHYPYAFIPFSAGLRNCIGQHFAIECKVAVALTLRLFKLAPDHS	480
Db	421	PQVFNPLRFSRENSSEKIHYPYAFIPFSAGLRNCIGQHFAIECKVAVALTLRLFKLAPDHS	480
Qy	481	RPPQPVRQVVLKSKNGIHVFAKKVC	505
Db	481	RPPQPVRQVVLKSKNGIHVFAKKVC	505

RESULT 2

AAE14447

ID AAE14447 standard; protein; 505 AA.

XX

AC AAE14447;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human drug metabolising enzyme (DME)-10.

XX

KW Human; drug metabolising enzyme; DME-10; autoimmune; inflammatory;
 KW cell proliferative; developmental; endocrine; eye; metabolic; AIDS;
 KW gastrointestinal disorder; liver disorder; cancer; arteriosclerosis;
 KW adult respiratory distress syndrome; anaemia; epilepsy; hypothyroidism;
 KW hypothalamus; pituitary; diabetes; hypogonadism; conjunctivitis;
 KW glaucoma; cystic fibrosis; hypercholesterolaemia; gastritis;
 KW peptic ulcer; hepatitis; gene therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .31

FT /label= Signal_peptide

FT Domain 14. .33

FT /label= Transmembrane_domain

FT Protein 32. .505

FT /label= Mature_DME-10

XX
 PN WO200190334-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 25-MAY-2001; 2001WO-US017150.
 XX
 PR 25-MAY-2000; 2000US-0207901P.
 PR 01-JUN-2000; 2000US-0208983P.
 PR 07-JUN-2000; 2000US-0209861P.
 PR 15-JUN-2000; 2000US-0211825P.
 PR 22-JUN-2000; 2000US-0213744P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Yue H, Sanjanwala MS, Baughn MR, Gandhi AR, Ring HZ, Elliott V;
 PI Walia NK, Yang J, Khan FA, Ramkumar J, Tang YT, Hafalia A, Lal P;
 PI Nguyen DB, Yao MG, Lee EA, Tribouley CM, Patterson C, Lu Y;
 PI Burford N, Ding L, Bruns CM, Kearney L, Reddy R;
 XX
 DR WPI; 2002-097650/13.
 DR N-PSDB; AAD24015.
 XX
 PT New human drug metabolizing enzymes and polynucleotides encoding the
 PT enzyme for diagnosing, preventing or treating cell proliferative,
 PT autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal
 PT disorders.
 XX
 PS Claim 1; Page 145-146; 158pp; English.
 XX
 CC The present sequence is human drug metabolising enzyme (DME)-10. DME
 CC polypeptide, polynucleotide and modulators are useful for diagnosis,
 CC treatment and prevention of autoimmune/inflammatory, cell proliferative,
 CC developmental, endocrine, eye, metabolic, and gastrointestinal disorders,
 CC including liver disorders. The autoimmune/inflammatory disorders
 CC treatable include AIDS, adult respiratory distress syndrome, Addison's
 CC disease, allergies, anaemia, asthma, atherosclerosis, osteoporosis,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, Crohn's disease,
 CC atopic dermatitis, diabetic mellitus, Graves' disease,
 CC glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus
 CC erythematosus, systemic sclerosis, ulcerative colitis, haemodialysis and
 CC uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic
 CC infections and trauma, and cell proliferative disorders such as cancer,
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis,
 CC cirrhosis, hepatitis and psoriasis. Developmental disorders include
 CC anaemia, renal tubular acidosis, epilepsy, hypothyroidism and cataract,
 CC and endocrine disorders include disorders of hypothalamus and pituitary,
 CC disorders associated with hypopituitarism, including sarcoidosis,
 CC diabetes insipidus, hypogonadism, disorders associated with
 CC hypothyroidism including goitre, acute thyroiditis, Graves' disease,
 CC disorders associated with hyperparathyroidism, pancreatic disorders such
 CC as type I or type II diabetes mellitus, disorders associated with
 CC adrenals such as hyperplasia, Cushing's disease, endometriosis,
 CC infertility, hypergonadal disorders, and gynaecomastia. Eye disorders
 CC include conjunctivitis, keratitis, glaucoma and macular degeneration, and
 CC metabolic disorders include diabetes, cystic fibrosis, goitre,
 CC hypercholesterolaemia, hypoglycaemia, hyperlipidaemia, lysosomal storage
 CC diseases, obesity, phenylketonuria and hypocalcaemia. Also the molecules
 CC are useful for treating gastrointestinal disorders such as dysphagia,
 CC gastritis, peptic ulcer, cholelithiasis, cirrhosis, hepatitis,
 CC hyperbilirubinaemia, constipation, diarrhoea, jaundice, Wilson's disease,

CC thrombosis and hepatic tumours. The DME polypeptide is also useful for
 CC screening its agonist or antagonist
 XX
 SQ Sequence 505 AA;

Query Match 100.0%; Score 2690; DB 5; Length 505;
 Best Local Similarity 100.0%; Pred. No. 1.2e-230;
 Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSWLQELMAHPFLLLLILLCSLLLLFQVIRLYQRRRWIRALHLFPAPPAHWFYGHKEF	60
Db	1	MEPSWLQELMAHPFLLLLILLCSLLLLFQVIRLYQRRRWIRALHLFPAPPAHWFYGHKEF	60
Qy	61	YPVKEFEVYHKLMEKYPCAVPLWVGPFMTMFFSVHDPDYAKILLKRQDPKSAVSHKILES	120
Db	61	YPVKEFEVYHKLMEKYPCAVPLWVGPFMTMFFSVHDPDYAKILLKRQDPKSAVSHKILES	120
Qy	121	VGRGLVTLDGSKWKKHRQIVKPGFNISILKIFITMSESVRMMLNKWEERIAQNSRLELF	180
Db	121	VGRGLVTLDGSKWKKHRQIVKPGFNISILKIFITMSESVRMMLNKWEERIAQNSRLELF	180
Qy	181	QHVSIMTLDSIMKCAFSHQSGIQLDSTLDSYLKAVFNLSKISNORMNFLHHNDLVFKFS	240
Db	181	QHVSIMTLDSIMKCAFSHQSGIQLDSTLDSYLKAVFNLSKISNORMNFLHHNDLVFKFS	240
Qy	241	SQGQIFSKFNQELHQFTEKVIQDRKESLKDCLKQDTPQRRWDFLDILLSAKSENTKDFS	300
Db	241	SQGQIFSKFNQELHQFTEKVIQDRKESLKDCLKQDTPQRRWDFLDILLSAKSENTKDFS	300
Qy	301	EADLQAEVKTFMFAGHDTTSSAISWILYCLAKYPEHQQRDEIRELLGDGSSITWEHLS	360
Db	301	EADLQAEVKTFMFAGHDTTSSAISWILYCLAKYPEHQQRDEIRELLGDGSSITWEHLS	360
Qy	361	QMPYTTMCIKECLRLYAPVVNISRLLDKPITFPDGRSLPAGITVFINIWALHHNPYFWED	420
Db	361	QMPYTTMCIKECLRLYAPVVNISRLLDKPITFPDGRSLPAGITVFINIWALHHNPYFWED	420
Qy	421	PQVFNPLRFSRENSEKIHYPYAFIPFSAGLRNCIGQHFAIECKVAVALTLLRFLAPDHS	480
Db	421	PQVFNPLRFSRENSEKIHYPYAFIPFSAGLRNCIGQHFAIECKVAVALTLLRFLAPDHS	480
Qy	481	RPPQPVRQVVLKSKNGIHVFAKKVC	505
Db	481	RPPQPVRQVVLKSKNGIHVFAKKVC	505

RESULT 3

ADU01526

ID ADU01526 standard; protein; 505 AA.

XX

AC ADU01526;

XX

DT 30-DEC-2004 (first entry)

XX

DE Breast cancer associated polypeptide seqid 307.

XX

KW cytostatic; gene therapy; vaccine; breast cancer; cancer; tumour;

KW immune response; O8E; vaccine.

XX

OS Homo sapiens.

XX